

FIGURE 1

TOOTEE BESTDOD

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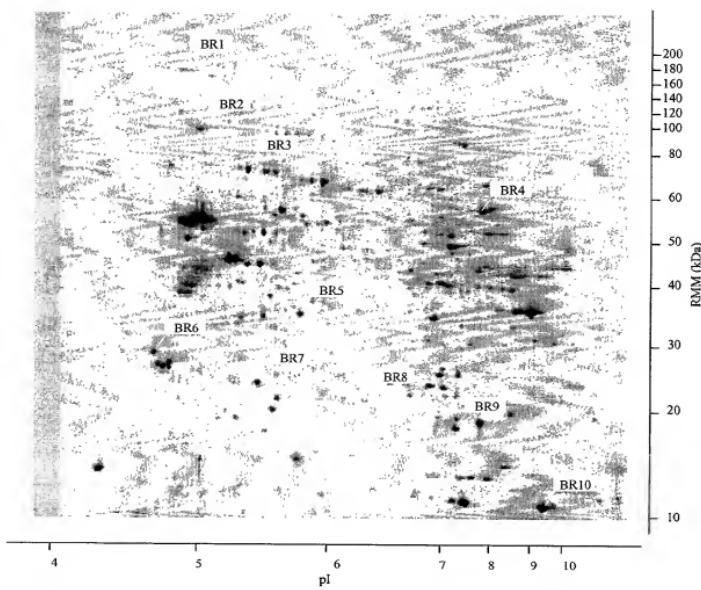


FIGURE 2.

Figure 2a

1 gtcggggacc atgtctggag aactaccacc aaacattaac atcaaggAAC
5 51 ctcgatggga tcaaagact ttcatGGAC gagccaatca ttcttcact
101 gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc
151 gagaaaaata gtacatgatt acaggcaagg aattgttctt cctggcttA
201 cagaaaatga attgtggaga gcaaagtaca tctatgatTC agctttcat
251 cctgacactg gtgagaagat gatTTGATA ggaagaatgt cagcccAGGT
301 tcccatgaac atgaccatCA caggTTgtat gatgacgTTT tacaggactA
351 cgccggcgtgt gctgttctgg cagtgGatta accagtcTT caatGCCGTC
401 gtcaattaca ccaacagaag tggagacgca cccctcaCTg tcaatgagtt
451 gggAACAGCT tacgttCTG caacaactgg tgccgtAGCA acagCTCTAG
501 gactcaatgc attgaccaag catgtcteac cactgatAGG acgtttgtt
551 ccctttGCTG ccgtAGCTG tgctaattGC attaatATTC cattaatGAG
601 gcaaaggGAA ctcaaAGTTG gcattCCeGT cacGGatGAG aatGGGAACC
651 gcttggggGA gtcggcGAAC gctgcgAAAC aagccatCAC gcaagttGTC
701 gtgtccAGGA ttctcatGGC agccccTGGC atggccatCC ctccattCAT
751 tatgaacACT ttggAAAAGA aagccTTTT gaagAGGATTC ccatGGATGA
20 801 gtgcacccat tcaagttGGG tttagttGGCT tctgtttGGT gtttgctACA
851 cccctgtgtt gtgcctgtt tcctcAGAAA agttccatGT ctgtgacaAG
901 cttggaggCC gagttGCAAG ctaAGATCCA agAGAGCCAT CCTGAATTGc
951 gacgcgtGTA cttaATAAG ggattGtaAA gcaggGAGGA aacctctGCA
1001 gtcattCTG ccactGAAA gctggGTGAG ccatGCTGGT gagaaaaATC
25 1051 ctgttcaacc tgggttctcc cagttacGGA aaggGCGAAT tcgcggccGc
1101 taattcgatt cgcctataG nagtnGtaAC antC

Figure 2b

1 MSGELPPNIN IKEPRWDQST FIGRANHFFT VTDPRNILLT NEQLESARKI
51 VHDYRQGIVP PGLTENELWR AKYIYDSAFH PDT GEKMILI GRMSAQVPMN
5 101 MTITGCNMTE YRTTPAVIEW QWINQSFNAV VNYTNRSGDA PLTVNELGTA
151 YVSATTGAVA TALGLNALTQ HVSPPLIGREV PFAAVAAANG INIPIPLMRQE
201 LKVGIPVTDE NGNRLLGESAN AAKQAITQVV VSRILMAAPG MATPFFIMNT
251 LEKKAFLKRF PWMSAPIQVG LVGFCLVFAF PLCCATFPQK SSMSVTSLEA
301 ELQAKIQESH PELRRVYFNK GL*

10 The tryptic peptides identified by mass spectrometry are underlined, motifs conserved in mouse sideroflexin
1 are boxed and sequences shaded in grey represent predicted transmembrane domains (Fleming *supra*)

FIGURE 3.

Figure 3a

1 gtccgggacc atgtctggag aactaccacc aaacattaac atcaaggAAC
5 51 ctcgatggga tcaaaggact ttcatggac gagccaatca tttcttcact
101 101 gtaactgacc ccaggaacat tctgttaacc aacgaacaac tcgagagtgc
151 151 gagaaaaata gtacatgatt acaggcaagg aattgttcct cctggctta
201 201 cagaaaatga attgtggaga gcaaagtaca tctatgatTC agctttcat
251 251 cctgacactg gtgagaagat gatTTGATA ggaagaatgt cagcccAGGT
301 301 tccccatgaac atgaccatca caggttgtat gatgacgttt tacaggactA
351 351 cgccggctgt gctgttctgg cagtgGATTa accAGTCTT caatGCCGTC
401 401 gtcaattaca ccaacagaag tggagacgca cccCTCACTG tcaatgagTT
451 451 gggaacagct tacgttctg taacaactgg tgccgtAGCA acagctctAG
501 501 gactcaatgc attgaccaag catgtctcac cactgatAGG acgtttgtt
551 551 ccctttgtg ccgttagctgc tgctaattGC attaatATTC cattaatGAG
601 601 gcaaAGCCAT ccctccATTC attatGAACA ctTTGGAAAA gaaAGCCTT
651 651 ttgaagaggt tccccatggat gagtgCACCC attcaAGTGT ggTTAGTGG
701 701 cttctgtttg gtgtttGCTA cacccCTGTG ttgtGCCCTG tttcCTcAGA
751 751 aaagttccat gtctgtgaca agcttggagg ccgagttgca agctaagatC
801 801 caagagagcc atcctgaatt gcgacgcgtg tacttcaata agggattgtA
851 851 aagcaggGAG gaaacctctG cagtcattc tgccactgca aagctggTGT
901 901 agccatgtG gtgagaaaaa tcctgttcaa cctgggttct cccagttANG
951 951 gaaaggGCGA attcgccGCC gctgattcna ttac

Figure 3b

5 MSGELPPNIN IKEPRWDQST FIGRANHFFT VTDPRNILLT NEQLESARKI
51 VHDYRQGIVP PGLTENELWR AKIYIYDSAHF PDTGEKMILI GRMSAQVPMN
101 MFTITGCMMTF YRTTPAVFEEQW OWINOSFNAV VNYTNRSGDA PLTVNELGTA
151 IVSVITIGAVA TALGLNALT K HVSPPLIGREV PFAAAVAAANG INPLMRQSH
201 PSIHYEHFGK ESLFEEVPMD ECTHSSWVSW LLFGVCYTPV LCPVSSEKFH
10 251 VCDKLGGRVA S*

The tryptic peptides identified by mass spectrometry are underlined, motifs conserved in mouse sideroflexin I are boxed and amino acids unique to this clone are shown in bold (all other amino acids are identical to the full length clone). sequences shaded in grey represent the predicted transmembrane domains.